

## SEQUENCE LISTING

&lt;110&gt; Bayer AG, BHC

&lt;120&gt; Method for inhibiting the replication of herpesviruses

&lt;130&gt; Le A 36 269

&lt;160&gt; 1

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1370

&lt;212&gt; PRT

&lt;213&gt; Human cytomegalovirus

&lt;400&gt; 1

```

Met Glu Asn Trp Ser Ala Leu Glu Leu Leu Pro Lys Val Gly Ile Pro
1      5      10      15
Thr Asp Phe Leu Thr His Val Lys Thr Ser Ala Gly Glu Glu Met Phe
20     25     30
Glu Ala Leu Arg Ile Tyr Tyr Gly Asp Asp Pro Glu Arg Tyr Asn Ile
35     40     45
His Phe Glu Ala Ile Phe Gly Thr Phe Cys Asn Arg Leu Glu Trp Val
50     55     60
Tyr Phe Leu Thr Ser Gly Leu Ala Ala Ala Ala His Ala Ile Lys Phe
65     70     75     80
His Asp Leu Asn Lys Leu Thr Thr Gly Lys Met Leu Phe His Val Gln
85     90     95
Val Pro Arg Val Ala Ser Gly Ala Gly Leu Pro Thr Ser Arg Gln Thr
100    105    110
Thr Ile Met Val Thr Lys Tyr Ser Glu Lys Ser Pro Ile Thr Ile Pro
115    120    125
Phe Glu Leu Ser Ala Ala Cys Leu Thr Tyr Leu Arg Glu Thr Phe Glu
130    135    140
Gly Thr Ile Leu Asp Lys Ile Leu Asn Val Glu Ala Met His Thr Val
145    150    155    160
Leu Arg Ala Leu Lys Asn Thr Ala Asp Ala Met Glu Arg Gly Leu Ile
165    170    175
His Ser Phe Leu Gln Thr Leu Leu Arg Lys Ala Pro Pro Tyr Phe Val
180    185    190
Val Gln Thr Leu Val Glu Asn Ala Thr Leu Ala Arg Gln Ala Leu Asn
195    200    205
Arg Ile Gln Arg Ser Asn Ile Leu Gln Ser Phe Lys Ala Lys Met Leu
210    215    220
Ala Thr Leu Phe Leu Leu Asn Arg Thr Arg Asp Arg Asp Tyr Val Leu
225    230    235    240
Lys Phe Leu Thr Arg Leu Ala Glu Ala Ala Thr Asp Ser Ile Leu Asp
245    250    255
Asn Pro Thr Thr Tyr Thr Thr Ser Ser Gly Ala Lys Ile Ser Gly Val
260    265    270
Met Val Ser Thr Ala Asn Val Met Gln Ile Ile Met Ser Leu Leu Ser
275    280    285
Ser His Ile Thr Lys Glu Thr Val Ser Ala Pro Ala Thr Tyr Gly Asn
290    295    300
Phe Val Leu Ser Pro Glu Asn Ala Val Thr Ala Ile Ser Tyr His Ser
305    310    315    320
Ile Leu Ala Asp Phe Asn Ser Tyr Lys Ala His Leu Thr Ser Gly Gln
325    330    335
Pro His Leu Pro Asn Asp Ser Leu Ser Gln Ala Gly Ala His Ser Leu
340    345    350
Thr Pro Leu Ser Met Asp Val Ile Arg Leu Gly Glu Lys Thr Val Ile

```

## SQL Le A 36 269

Met	Glu	Asn	Leu	Arg	Arg	Val	Tyr	Lys	Asn	Thr	Asp	Thr	Lys	Asp	Pro
355	370					360					365				
Leu	Glu	Arg	Asn	Val	Asp	Leu	Thr	Phe	Phe	Phe	Pro	Val	Gly	Leu	Tyr
385					390					395					400
Leu	Pro	Glu	Asp	Arg	Gly	Tyr	Thr	Thr	Val	Glu	Ser	Lys	Val	Lys	Leu
			405						410					415	
Asn	Asp	Thr	Val	Arg	Asn	Ala	Leu	Pro	Thr	Thr	Ala	Tyr	Leu	Leu	Asn
			420					425					430		
Arg	Asp	Arg	Ala	Val	Gln	Lys	Ile	Asp	Phe	Val	Asp	Ala	Leu	Lys	Thr
		435					440					445			
Leu	Cys	His	Pro	Val	Leu	His	Glu	Pro	Ala	Pro	Cys	Leu	Gln	Thr	Phe
	450					455					460				
Thr	Glu	Arg	Gly	Pro	Pro	Ser	Glu	Pro	Ala	Met	Gln	Arg	Leu	Leu	Glu
465					470					475					480
Cys	Arg	Phe	Gln	Gln	Glu	Pro	Met	Gly	Gly	Ala	Ala	Arg	Arg	Ile	Pro
			485						490					495	
His	Phe	Tyr	Arg	Val	Arg	Arg	Glu	Val	Pro	Arg	Thr	Val	Asn	Glu	Met
			500					505					510		
Lys	Gln	Asp	Phe	Val	Val	Thr	Asp	Phe	Tyr	Lys	Val	Gly	Asn	Ile	Thr
		515					520					525			
Leu	Tyr	Thr	Glu	Leu	His	Pro	Phe	Phe	Asp	Phe	Thr	His	Cys	Gln	Glu
	530					535					540				
Asn	Ser	Glu	Thr	Val	Ala	Leu	Cys	Thr	Pro	Arg	Ile	Val	Ile	Gly	Asn
545					550					555					560
Leu	Pro	Asp	Gly	Leu	Ala	Pro	Gly	Pro	Phe	His	Glu	Leu	Arg	Thr	Trp
			565						570					575	
Glu	Ile	Met	Glu	His	Met	Arg	Leu	Arg	Pro	Pro	Pro	Asp	Tyr	Glu	Glu
			580					585					590		
Thr	Leu	Arg	Leu	Phe	Lys	Thr	Thr	Val	Thr	Ser	Pro	Asn	Tyr	Pro	Glu
		595					600					605			
Leu	Cys	Tyr	Leu	Val	Asp	Val	Leu	Val	His	Gly	Asn	Val	Asp	Ala	Phe
	610					615					620				
Leu	Leu	Ile	Arg	Thr	Phe	Val	Ala	Arg	Cys	Ile	Val	Asn	Met	Phe	His
625					630					635					640
Thr	Arg	Gln	Leu	Leu	Val	Phe	Ala	His	Ser	Tyr	Ala	Leu	Val	Thr	Leu
			645						650					655	
Ile	Ala	Glu	His	Leu	Ala	Asp	Gly	Ala	Leu	Pro	Pro	Gln	Leu	Leu	Phe
		660						665					670		
His	Tyr	Arg	Asn	Leu	Val	Ala	Val	Leu	Arg	Leu	Val	Thr	Arg	Ile	Ser
		675					680					685			
Ala	Leu	Pro	Gly	Leu	Asn	Asn	Gly	Gln	Leu	Ala	Glu	Glu	Pro	Leu	Ser
	690					695					700				
Ala	Tyr	Val	Asn	Ala	Leu	His	Asp	His	Arg	Leu	Trp	Pro	Pro	Phe	Val
705					710					715					720
Thr	His	Leu	Pro	Arg	Asn	Met	Glu	Gly	Val	Gln	Val	Val	Ala	Asp	Arg
			725						730					735	
Gln	Pro	Leu	Asn	Pro	Ala	Asn	Ile	Glu	Ala	Arg	His	His	Gly	Val	Ser
			740					745					750		
Asp	Val	Pro	Arg	Leu	Gly	Ala	Met	Asp	Ala	Asp	Glu	Pro	Leu	Phe	Val
		755					760					765			
Asp	Asp	Tyr	Arg	Ala	Thr	Asp	Asp	Glu	Trp	Thr	Leu	Gln	Lys	Val	Phe
	770					775					780				
Tyr	Leu	Cys	Leu	Met	Pro	Ala	Met	Thr	Asn	Asn	Arg	Ala	Cys	Gly	Leu
785					790					795					800
Gly	Leu	Asn	Leu	Lys	Thr	Leu	Leu	Val	Asp	Leu	Phe	Tyr	Arg	Pro	Ala
			805						810					815	
Phe	Leu	Leu	Met	Pro	Ala	Ala	Thr	Ala	Val	Ser	Thr	Ser	Gly	Thr	Thr
			820					825					830		
Ser	Lys	Glu	Ser	Thr	Ser	Gly	Val	Thr	Pro	Glu	Asp	Ser	Ile	Ala	Ala
		835					840					845			
Gln	Arg	Gln	Ala	Val	Gly	Glu	Met	Leu	Thr	Glu	Leu	Val	Glu	Asp	Val
	850					855					860				

## SQL Le A 36 269

Ala Thr Asp Ala His Thr Pro Leu Leu Gln Ala Cys Arg Glu Leu Phe  
 865 870 875 880  
 Leu Ala Val Gln Phe Val Gly Glu His Val Lys Val Leu Glu Val Arg  
 885 890 895  
 Ala Pro Leu Asp His Ala Gln Arg Gln Gly Leu Pro Asp Phe Ile Ser  
 900 905 910  
 Arg Gln His Val Leu Tyr Asn Gly Cys Cys Val Val Thr Ala Pro Lys  
 915 920 925  
 Thr Leu Ile Glu Tyr Ser Leu Pro Val Pro Phe His Arg Phe Tyr Ser  
 930 935 940  
 Asn Pro Thr Ile Cys Ala Ala Leu Ser Asp Asp Ile Lys Arg Tyr Val  
 945 950 955 960  
 Thr Glu Phe Pro His Tyr His Arg His Asp Gly Gly Phe Pro Leu Pro  
 965 970 975  
 Thr Ala Phe Ala His Glu Tyr His Asn Trp Leu Arg Ser Pro Phe Ser  
 980 985 990  
 Arg Tyr Ser Ala Thr Cys Pro Asn Val Leu His Ser Val Met Thr Leu  
 995 1000 1005  
 Ala Ala Met Leu Tyr Lys Ile Ser Pro Val Ser Leu Val Leu Gln  
 1010 1015 1020  
 Thr Lys Ala His Ile His Pro Gly Phe Ala Leu Thr Ala Val Arg  
 1025 1030 1035  
 Thr Asp Thr Phe Glu Val Asp Met Leu Leu Tyr Ser Gly Lys Ser  
 1040 1045 1050  
 Cys Thr Ser Val Ile Ile Asn Asn Pro Ile Val Thr Lys Glu Glu  
 1055 1060 1065  
 Arg Asp Ile Ser Thr Thr Tyr His Val Thr Gln Asn Ile Asn Thr  
 1070 1075 1080  
 Val Asp Met Gly Leu Gly Tyr Thr Ser Asn Thr Cys Val Ala Tyr  
 1085 1090 1095  
 Val Asn Arg Val Arg Thr Asp Met Gly Val Arg Val Gln Asp Leu  
 1100 1105 1110  
 Phe Arg Val Phe Pro Met Asn Val Tyr Arg His Asp Glu Val Asp  
 1115 1120 1125  
 Arg Trp Ile Arg His Ala Ala Gly Val Glu Arg Pro Gln Leu Leu  
 1130 1135 1140  
 Asp Thr Glu Thr Ile Ser Met Leu Thr Phe Gly Ser Met Ser Glu  
 1145 1150 1155  
 Arg Asn Ala Ala Ala Thr Val His Gly Gln Lys Ala Ala Cys Glu  
 1160 1165 1170  
 Leu Ile Leu Thr Pro Val Thr Met Asp Val Asn Tyr Phe Lys Ile  
 1175 1180 1185  
 Pro Asn Asn Pro Arg Gly Arg Ala Ser Cys Met Leu Ala Val Asp  
 1190 1195 1200  
 Pro Tyr Asp Thr Glu Ala Ala Thr Lys Ala Ile Tyr Asp His Arg  
 1205 1210 1215  
 Glu Ala Asp Ala Gln Thr Phe Ala Ala Thr His Asn Pro Trp Ala  
 1220 1225 1230  
 Ser Gln Ala Gly Cys Leu Ser Asp Val Leu Tyr Asn Thr Arg His  
 1235 1240 1245  
 Arg Glu Arg Leu Gly Tyr Asn Ser Lys Phe Tyr Ser Pro Cys Ala  
 1250 1255 1260  
 Gln Tyr Phe Asn Thr Glu Glu Ile Ile Ala Ala Asn Lys Thr Leu  
 1265 1270 1275  
 Phe Lys Thr Ile Asp Glu Tyr Leu Leu Arg Ala Lys Asp Cys Ile  
 1280 1285 1290  
 Arg Gly Asp Thr Asp Thr Gln Tyr Val Cys Val Glu Gly Thr Glu  
 1295 1300 1305  
 Gln Leu Ile Glu Asn Pro Cys Arg Leu Thr Gln Glu Ala Leu Pro  
 1310 1315 1320  
 Ile Leu Ser Thr Thr Thr Leu Ala Leu Met Glu Thr Lys Leu Lys  
 1325 1330 1335  
 Gly Gly Ala Gly Ala Phe Ala Thr Ser Glu Thr His Phe Gly Asn

